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April 28, 2004, 10:12:24 ; Search time 54 Seconds (without alignments) 4871.350 Million cell updates/sec
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1 MSSGLWSQEKVTSPYWEERI......RLLCDAYMCMYQSPTWSLYK 949
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_MRW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

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5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1138120 seqs, 277189581 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4, Appli Sequence 1609, Ap Sequence 1610, Ap Sequence 120, Ap Sequence 2751, Ap Sequence 2751, Ap Sequence 2990, Ap Sequence 857, App Sequence 66115, A Sequence 6116, Ap Sequence 731, App Sequence 731, App Sequence 731, App Sequence 731, App Sequence 5606, Ap
SUMMARIES	US-09-851-673-4 US-10-264-237-1609 US-10-264-237-1610 US-09-864-761-34675 US-10-087-192-120 US-10-108-260A-2751 US-10-104-047-2990 US-09-764-875-857 US-10-282-122A-66115 US-09-764-868-731 US-09-764-868-731 US-10-106-698-5606 US-10-106-698-5606 US-10-087-192-117 US-10-087-192-117
DB	1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2 2 1 1 2
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Sequence 50, Appl Sequence 16, Appl Sequence 51, Appli Sequence 51, Appli Sequence 512, Appl Sequence 33, Appl Sequence 1945, Appl Sequence 1945, Appl Sequence 75, Appl Sequence 75, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 117, Appli Sequence 117, Appli Sequence 117, Appli Sequence 11, Appli Sequence 11, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 27, Appli Sequence 27, Appli Sequence 57, Appli Sequence 27, Appli	
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APPLICANT: Description, William
APPLICANT: Panslow, William
APPLICANT: Panslow, William
APPLICANT: Dougall, William
APPLICANT: Dougall, William
APPLICANT: Dougall, William
APPLICANT: Dougall, William
APPLICATION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING FILE REPERENCE: 3198
CURRENT APPLICATION NUMBER: US/09/851,673
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.8%; Score 4971.5;
99.2%; Pred. No. 0;
iive 0; Mismatches
                   ; Sequence 4, Application US/09851673; Publication No. US20030165985A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.8
Best Local Similarity 99.2
Matches 948; Conservative
                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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US-09-851-673-4
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181 YQGKQLFQCDEDCGVFVALDKLELIEDDDTALESDYAGPGDTMQVELPPLEINSRVSLKV, 240
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                                                                                          DIIP---ESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNR-RSELFYTLNG
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APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAISIBL

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT PILING DATE: 2002-10-04

PRIOR PELING DATE: 2001-05-18

PRIOR PELING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PATENTIN VET: 3.1

SEQ ID NO 1609

LENGTH: 261
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; Publication No. US20040009491A1
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ORGANISM: Homo sapiens
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LOCATION: (209)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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NAME/KEY: MISC FEATURE
LOCATION: (257)
COTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1609
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Sequence 1610, Application US/10264237

Bublication No. US20040009491A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA131P1

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/16450

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 1610

LENGTH: 238
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Pred. No. 2e-103;
0; Mismatches 3;
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Pred. No. 1.7e-94;
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98.2%;
                                                                                                                                                                                                                                                                                                                                                                           Query Match 25.3%;
Best Local Similarity 98.7%;
Matches 234; Conservative
                                                                   NAME/KEY: MISC FEATURE LOCATION: (218)
OTHER INFORMATION: Xaa
                                                                                                                                    FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (227)
OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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NAME/KEY: MISC FEATURE
-----TON: (227)
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-264-237-1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 KPKATGSTSDPGNRRSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFD 389
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                                                                                                  N: EXPRESSED IN BT474, SIGNAL = 0.98

N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.92

N: EXPRESSED IN HELLO, SIGNAL = 1.5

N: EXPRESSED IN HELLO, SIGNAL = 1.3

N: EXPRESSED IN HELA, SIGNAL = 1.3

N: EXPRESSED IN HEACHT, SIGNAL = 0.89

N: EXPRESSED IN LUNG, SIGNAL = 1

N: EXPRESSED IN LUNG, SIGNAL = 1

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.3

N: EXPRESSED IN BRAIN, SIGNAL = 1.4

N: EXPRESSED IN BRAIN, SIGNAL = 1.4
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APPLICANT: Morris, David W.
APPLICANT: Morris, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: CANCER
TITLE REPRESENCE: 529452000122
CURRENT APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.9%; Score 146; DB 12;
20.4%; Pred. No. 0.00098;
tive 48; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.9%; Score 597; DB 9; 1
100.0%; Pred. No. 2.6e-44;
ive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120
LENGTH: 354
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Publication No. US20020182586A1
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Best Local Similarity 20.43
Matches 89; Conservative
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Best Local Similarity 100.
Matches 113; Conservative
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US-10-087-192-120
                                                                                                  OTHER INFORMATION: E OTHER INFORMATION: E
                                 PEATURE:
CTHER INFORMATION: OTHER INFORMATION:
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OTHER INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
APPLICANT: HANZEL, David K.
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/532,366
                                                                                                                                                                538
                                                                                                                                                                                            61 GVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKKALFVKLKSCRPDSRF 120
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                                                                                                        1 MPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMXPGNSHGLEVGSLAEVKENPPFY
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                                                     419 MPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKENPPFY
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                TLFCLFAFSSVLDTVLLRPKEKNDVEYYSETQELLRTEIVNPLRIYGY 646
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Indels
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4,
Mismatches
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
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APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: PCT/US01/00668
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PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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APPLICATION NUMBER: US 60/236,359
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Patent No. US20020048763A1
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PRIOR APPLICATION NUMBER: GB 24263.6
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Matches 224; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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TITLE OF INVENTION: CYTOSKELETON-ASSOCIATED PROTEINS
FILE REFERENCE: PF-0772 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.0%; Score 143; DB 16;
21.0%; Pred. No. 0.0038;
                                                                                                                                                                             457 HDGSVFGVRYFTCPPRHGVFA-----PASR 481
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; OTHER INFORMATION: Incyte ID No: 1295420CD1
US-10-275-595A-13
                                                                                                              507 TDGTFRGTRYFTCALKKALFVKLKSCRPDSR
                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/10275595A
Publication No. US20040078804A1
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AU-YOUNG, Janice
LU, Dyung Aina M.
BAUGHN, Mariah R.
HILLMAN, Jennifer L.
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Best Local Similarity 21.0%
Matches 120; Conservative
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YAO, Monique G.
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BURFORD, Neil
BATRA, Sajeev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEARNEY, Liam
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                 TFRGTRYFTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVVBENTP 569
                                                                                                                                                                                                                                                   ---PVHKVTKIGF-----PSTTP 292
                                                                                                                                                                                                                                                                                                                         PKMEKEGL-EIMIGKKKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEYYSE 628
                                                                                                                                                                                                                                                                                                                                                                             293 AKAKANAVRRVWATTSASLKRSPSASSLSS------335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |::| |::| : |: |: DPACQEILFDPQTTIPELF---AIVRQWVPQVQHKIDVIGNEILRRGCHVNDRDGLTDMT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------PHAVLFVDEDVVEINEKFTELLLAITNCEERFSLFKNRNLSKGL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIDVGCPVKVQLRSGEEKFPGVVR----FRGPLLAERTVSGIFFGVE--LLEEGRGQGF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 YFDVPDLVRVLLKGAR---PRVVNSTCSDFNHGSALHIAASSLCLGAAKCLLEHGANPAL 226
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                                 SPPLAMPPGNSHGLEVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDG
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21.0%; Pred. No. 0.0038;
iive 59; Mismatches 174; Indels 218;
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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVERTION: No. US20040005560Alel full length cDNA
FILE REFERENCE: H1-A0106
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CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOCTWARE: Patentin Ver. 2.1
SEQ ID NO 2751
LENGTH: 547
                                                                                                                                                                                                                                                   260 AVAĞTRYFQCQPKYGLFA----
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----RTGLVRPLSHY 346
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Matches 120; Conservative
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CORGANISM: Homo sapiens
US-10-108-260A-2751
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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Zyskind, Judith
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Best Local Similarity 23.1
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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    RESULT 9
US-09-764-875-857
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285 GNLMLSAL-GLRIGDRVILDGQKT---GTLRFCGTT--EFASGQWVGVELDEPEGKNDGS 338
                                                                                                                                                                                416
                                                                                                                                                                                                                                                                                                                         134 PKTPRMDF-SRVTG-KGRREHKGKKKTPSSPSLGSLQQ-------------------169
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                                                            278 FDGV---LCS----FACVESTILLHINDIIPESVTQERRPPKLAFMSRGVGDKGSSSHN 329
                                                                                                                                         330 KPKATGSTSDPGNRRSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFD 389
                                                                                                                                                                                                                    390 RSSPPLOPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAOSVMEELNTAPVOE 449
                                                                                                                                                                                                                                                            ----- 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 KESLGYFVGVDMDNPIGNWDGRFDGV---LCS----FACVESTILLHINDIIPESVTQE 307
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                                                                                                 339 VGGVRYFICPPKOGLFASVSK--ISKAVDAPPSSVTSTPRTPRMDF-SRVTG-KGRREHK 394
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                                                                                                                                                                              395 GKKKTPSSPSLGSLQQ-----------RDGAKA------
                                                                                                                                                                                                                                                                                                 450 SPPLAMPPGNSHGLEVGS---LAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90; Indels 153;
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CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR PILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Atentin Ver. 2.1
SEQ ID NO 2990
LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                            507 TDGTFRGTRYFTCALKKALFVKLKSCRPDSR 537
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457 HDGSVFGVRYFTCPPRHGVFA-----PASR 481
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ORGANISM: Homo sapiens
US-10-104-047-2990
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NAME/KEY: SITE
LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (358)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 SGCSPRDSGCYESSENLENGKTRKASLLSAKSSTEPSLKSFSRNOLGNY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 ACVESTILLHINDIIPESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 TAPVQESPPL-----AMPPGNSHGLEVGSLAEVKENPPFYGVIRWIGQPPGLN 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 857, Application US/09764875;
Publication No. US20040018969A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
PILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/764,875
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper;
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.7%; Score 135.5; DB 11; Length 721; 23.1%; Pred. No. 0.028; tive 44; Mismatches 132; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 66115, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
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1761 SAKD--DELNEKYRSERIEKGETFKEANLNQNNAGGLKFGLKQNDIHSNDKYALAKMGLG 1818
                                                                            : | | :: | :: | :: | :: | BELLIKEVELNRDVAK------EFINETLIGGIADEAYRSQFIAEHRLMTFKMDEN 1922
                                                                                                                                                                                                                                                                            -------FDNSVKLKKEFASFKDYWEAYKAIGGNIYELR 1970
                                                                                                                                                                                                                                                                                                                                                      288 LPVSICRSCETLEGPQTVDTWPRSHSLDDLQVEPGAEQDVPTEVTEPPPQIVPEVPQKTT 347
                                                                                                                                                                                                                              TPPKMEKEGLEIMIGKKKGIQGHYNSCYLDSTLFCLFAFSSVLD------TVLLRPK 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 E-INSRVS--LKGGETIESGTVIFCDVLPGKESLGYFVGVDMDNPIGNWDGRFDGVLCSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 ACVESTILLHINDIIPESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRRS 345
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                                               467 -SLAEVKENPPFYGVIRWIGQPPGLNE---VLAGLELEDECAGCTDGTFRGTRYFTCALK 522
                                                                                                                                                                                                                                                                                                                           EKNDVEYYSETQELLRTEIVNPLRIYGYVCATKIMKLRKILEKVEAASGFTSEEK----D
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Patent No. US20020168711A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: NUCLEIC ACIDS, Proteins, and Antibodies
FILE REFERENCE: PT232

CURRENT PELLING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 1510

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 731

LENGTH: 721
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23.1%; Pred. No. 0.034;
ive 44; Mismatches 132;
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Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 KFTELLLAITNC----EERFSLFKNRNRLSKGLQIDV-------GCPVKVQLRS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----QLFQCDEDCGF---VALDKLELIEDDDTALESDYA---GPGDTMQVE 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 LCSFACVESTILLHINDIIPESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --NRRSELF----YTLN-----GSSVDSQPQSKSKN-----TWYID-EVAEDPAK 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTQKLLKVPKGSIGQYIQDRSVGHSRIPSAKGKKNQIGLKILEQPHAVLFVDEDVVEINE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEEKFPGVVRFRGPLLAERTVSGIFFG--VELLEEGRGQGFT-----DGVYQGK----
                       APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLTEISTDFDRSSPPLQPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPLSL----
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                                                              FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-06

PRIOR PILING DATE: 2000-05-06

PRIOR PILING DATE: 2000-05-06

PRIOR PILING DATE: 2000-05-09

PRIOR PILING DATE: 2000-01-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09
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SEQ ID NO 66115
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FEATURE:
NAMB/KEY: MISC FEATURE
LOCATION: (147)
OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC FEATURE
LOCATION: (300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-5606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 DIMQVELPPLEINSRVSLKG------GETIESGTVIFCDVLPGKESLGYFVGVDMDN 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 PIGNWDGRFDGVLCSFACVESTILLHINDIIPESVTQERRPPKLAFMSRGVGDKGSSSHN 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 PIGKNDGSVAGVR-YFQCEP-----LKGIF-----TRPSKL---TRKV------QA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 KPKATGSTSDPGNRRSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFD 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   390 RSSPPLQPPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQE 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 SPPLAMPPGNSHGLEVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.7%; Score 134; DB 14; Length 307; Best Local Similarity 22.1%; Pred: No. 0.0088; Matches 70; Conservative 35; Mismatches 110; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MOLILA, DAYLER, APPLICANT: BENGELIARD, BENGELIARD, ENGER TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER FILE REFERENCE: 529452000122 CURRENT APPLICATION NUMBER: US/10/087,192 CURRENT FILING DATE: 2002-03-01 PRIOR FILING DATE: 2001-12-22 PRIOR FILING DATE: 2001-12-22 PRIOR FILING DATE: 2001-03-02 PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(439)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-087-192-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 117, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
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180 -AKEPSATPPISNLT-----
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PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8664
SOFTWARE: PATENTIN VEr. 3.0
SEQ ID NO 5606
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                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REPERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR PILING DATE: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: US 60/163,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-875-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 SGCSPRDSGCYESSENLENGKTRKASLLSAKSSTEPSLKSFSRNQLGNY----- 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 GFVALDKLELIEDDD------TALE-----SDYAGPGDTMQVELPPL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 E-INSRVS--LKGGETIESGTVIFCDVLPGKESLGYFVGVDMDNPIGNWDGRFDGVLCSF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ELFYTING-SSVDSQPQSKSKNTWYID-----EVAEDPAKSLTEISTDFD 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 GYEDLDTFKLLEEEDLDELNIRDPEHRAVLLTAVELLQEYDSNSDQSGSQEKLLVDSQGL 191
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                                                                            -----SPPQCLPRNYDAQPPGAKHGLARTPLEGHRKGHEFEGTHHPLGTKEGVD 445
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                                                                                                                                                                                                                           Sequence 1140. Application US/09764875

Sequence 1140. Application US/09764875

Publication No. US20040018969A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUZOZ

CURRENT APPLICATION NUMBER: US/09/764,875

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1249

SOFTWARE: PatentIn Ver. 2.0
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 82; Conserva
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Kianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REPERENCE: 38-10 (52052) B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2000-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 717
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                                                                                                                                                                                                                     295 HINDIIPESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRRSELFYTLNGS 354
                                                                                                                                                                                                                                                                                            SVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSLTTENRFHSLPF 414
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                                                                                               78 IQFLGET-----QFAPGQ-----WAGIVLDEPIGKNDGSVAGVR-YFQCEP----
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                                                                         ELIEDDDTALESDYA-----GP--GP--GDTMQVELPPLEINSRVSLKG----
                                       Gaps
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Query Match 2.6%; Score 132.5; DB 12; Length 439; Best Local Similarity 20.2%; Pred. No. 0.022; Matches 107; Conservative 63; Mismatches 182; Indels 179;
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US-10-369-493-22287
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Best Local S:
Matches 84,
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ORGANISM:
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Scoring table:

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Sequence 18843, As Sequence 2399, Ap Sequence 2399, Ap Sequence 2391, Ap Sequence 5971, Ap Sequence 1207, Ap Sequence 1207, Ap Sequence 1209, Ap Sequence 1609, Ap Sequence 1609, Ap Sequence 1609, Ap Sequence 1610, Ap
  Sequence 3, Appli
Sequence 137, App
Sequence 137, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 490, App
Sequence 490, App
Sequence 1743, Ap
Sequence 1743, Ap
Sequence 1743, Ap
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Sequence 26809, A
Sequence 21147, A
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Sequence 9570, Ap
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Sequence 15308, 7
Sequence 27668, 7
DECT-USO2-27777-137
PCTT-USO2-17777-137
PCTT-USO2-17777-137
PCTT-USO2-17777-137
PCTT-USO2-17777-137
PCTT-USO2-1777-137
PCTT-USO2-1777-137
PCTT-USO2-14570-4
PCT-USO1-01239-1743
PCTT-USO1-01239-1743
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PCTT-USO1-01239-1743
PCTT-USO1-16450-18843
PCTT-USO1-16450-18893
PCTT-USO1-16450-1609
PCTT-USO1-16450-1609
PCTT-USO1-16450-1610
PCTT-USO1-16450-1739
PCTT-USO1-16450-1610
PCTT-USO1-16450-1610
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: KOVALENKO, Andrei
APPLICANT: KOVALENKO, Andrei
APPLICANT: CANTARELLA, Giuseppina
ITILE OF INVENTION: INHIBITOR OF NF-KB ACTIVATOR
FILE REFERENCE: WALLACH=25
CURRENT FILING DATE: 2000-09-28
FRIOR APPLICATION NUMBER: US/09/671,687A
CURRENT FILING DATE: 2000-09-18
FRIOR FILING DATE: 2000-09-18
FRIOR FILING DATE: 1996-09-01
FRIOR FILING DATE: 1996-09-01
FRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-864-761-34675
US-10-182-993-26809
US-10-182-995-21147
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TYPE: PRT
ORGANISM: Homo sapiens
       RESULT 1
US-09-671-687A-3
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1: (cgn2 6/ptodata/2/paa/BCTUS COMB.pep:*
2: (cgn2 6/ptodata/2/paa/USO6 COMB.pep:*
3: (cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
4: (cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
6: (cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
7: (cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
8: (cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
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16: (cgn2 6/ptodata/2/paa/USO8 COMB.pep:*
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20: (cgn2 6/ptodata/2/paa/USO0 COMB.pep:*
20: (cgn2 
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                          MSSGLWSQEKVTSPYWEERIFYLLLQECSVTDKQTQKLLKVPKGSIGQYIQDRSVGHSRI
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                                                              MSSGLWSQEKVTSPYWEER1FYLLLQECSVTDKQTQKLLKVPKGSIGQYIQDRSVGHSRI
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                    Length 949;
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                     DB 20;
                                          0; Mismatches
                     Score 5034;
Pred. No. 0;
                    100.0%;
                              Local Similarity 100.
nes 949; Conservative
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                               APPLICANT: dialbeaus, Inc.
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Salceda, Susana
TITLE OF INVENTION: Compositions and Methods Rel
FILE REPERENCE: DEX-0346
CURRENT APPLICATION NUMBER: PCT/US02/27777
CURRENT FILING DATE: 2002-08-29
PRIOR PLILING DATE: 2001-08-29
PRIOR PLILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.1
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Pred. No. 0;
Sequence 137, Application PC/TUS0227777
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%;
99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.5
Matches 948; Conservative
                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapien
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RESULT 2 PCT-US02-27777-137

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APPLICANT: IMMUNEX CORPORATION
APPLICANT: IMMUNEX CORPORATION
APPLICANT: Enablow III, William
APPLICANT: Enablow III, William
APPLICANT: Dougall, William C.
TITLE OF INVENTION: SCREENING ASSAYS FOR AGONISTS OR ANTAGONISTS OF CD40 SIGNALING
FILE REFERENCE: 3198-WO
CURRENT PAPLICATION NUMBER: PCT/US02/14570
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 09/851,673
PRIOR APPLICATION NUMBER: 09/851,673
SPRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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Pred. No. 0;
0; Mismatches
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99.2%;
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Best Local Similarity 99.2
Matches 948; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Salceda. Susana
TITLE OF INVENTION: Compositions and Methods related to Breast Specific Genes and F
FILE REFERENCE: DEX-0346
CURRENT APPLICATION NUMBER: PCT/US02/27777A
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 60/316,307
PRIOR APPLICATION NUMBER: US 60/316,307
SEQ ID NOS: 170
SOFTWARE: Patentin Version 3.1
SEQ ID NO 137
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                                              TPROCRICGGLAMY ECRECYDDPD I SAGKI KOPCKTCNTOVHLHPKRLNHKYNPVSLPKD
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Pred. No. 0;
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Best Local Similarity 99.5
Matches 948; Conservative
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ORGANISM: Homo sapien
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Sequence 490, Application US/10755889
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB

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PKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDSMADRDGGQNG
                                                                       841 PKDLPDWDWRHGCIPCQNMELFAVLCIETSHYVAFVKYGKDDSAWLFFDSWADRDGGQNG
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                                                                                                                FNIPQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSPTMSLYK 949
                                                                                                                                 FNIPQVTPCPEVGEYLKMSLEDLHSLDSRRIQGCARRLLCDAYMCMYQSPTMSLYK 956
                                                                                                                                                                                                                                                                         APPLICANT: CARMAN, JULIE
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH
TITLE OF INVENTION: NF-KB PATHWAY
FILE REPERRINCE: 3053-4191
CURRENT FILLING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 746
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 990
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Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                           APPLICANT: NADLER, STEVEN G.
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Best Local Similarity 99.2
Matches 948; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-60-440-068-490
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US-60-440-068-490
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Pred. No. 0;
0; Mismatches
TITLE OF INVENTION: PATHWAY
FILE REFERENCE: DO284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR PLING DATE: 2003-01-14
PRIOR PLING DATE: 2003-05-12
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                          98.8%;
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Best Local Similarity 99.2
Matches 948; Conservative
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; ORGANISM: Homo sapiens
US-10-755-889-490
                                                                                                                                                           SEQ ID NO 490
LENGTH: 956
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1743
LENGTH: 739
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ13PCT
CURRENT APPLICATION NUMBER: PCT/US01/01239
CURRENT FILING DATE: 2001-01-17
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Best Local Similarity 95.7
Matches 736; Conservative
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; ORGANISM: HOMO PCT-US01-01239-1743
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GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB;
TITLE OF INVENTION: PATHWAY
FILE REFERENCE: D0284 PSP1
CURRENT APPLICATION NUMBER: US/60/469,757
CURRENT PILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTIN VERSION 3.2
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                                            KNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDL
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Pred. No. 0;
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-60-469-757-490
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US-60-469-757-490
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GENERAL INFORMATION:
APPLICANT: INCTTE PHARMACEUTICALS, INC.
APPLICANT: TANG, Y. Tom
APPLICANT: TANG, Y. Tom
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: APPLICANT: AZIMZAI, Yald
APPLICANT: AZIMZAI, Yalda
APPLICANT: BAUGHN, Mariah R.
TITLE OF INVENTION: HUMAN CYTOSKELETON ASSOCIATED PROTEIN
FILE REFERENCE: PF-0594 PCT
CURRENT APPLICATION NUMBER: US/09/786, 797B
CURRENT FILING DATE: 1998-09-18; 1998-09-18; 1999-04-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PERL PROGram
SEQ ID NO 9
LENGTH: 731
TYPE: PRT
CREATURE:
CREATURE:
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 ESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRNRSELFYTLNGSSVDSQP
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                                  QSKSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSLTTENRFHSLPFSLTKMP
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT213
CURRENT APPLICATION NUMBER: US/09/764,902
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapp SOFTWARE: Patentin Ver. 2.0
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; Pred. No. 0;
0; Mismatches
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GENERAL INFORMATION:
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95.7%;
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Best Local Similarity 95.7
Matches 736; Conservative
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US-09-764-902-1743
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RESULT 13
US-09-629-469A-18843
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                                                                                                         MQVELPPLEINSRVSLKVGETIESGTVIFCDVLPGKESLGYFVGVDMDNPIGNWDGRFDG
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                                                                      Gaps
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                                               Length
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APPLICANT: Lal, Preeti
APPLICANT: Yue, Henry
APPLICANT: Hilman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Azimzai, Yalda
APPLICANT: Azimzai, Yalda
APPLICANT: Baughn, Mariah R.
TITLE OP INVENTION: HUMAN CYTOSKELETAL PROTEINS
                                               DB
                                            Score 3862; DB Pred. No. 0; 0; Mismatches
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2363327
US-09-786-797B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-60-131-321-7; Sequence 7, Application US/60131321; GENERAL INFORMATION:
                                            Query Match
Best Local Similarity 99.6%;
Matches 728; Conservative
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                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                       DB 33;
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Pred. No. 0;
0; Mismatches
FILE REFERENCE: PF-0692 P
CURRENT APPLICATION NUMBER: US/60/131,321
CURRENT FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 7.
                                                                                                                                                                                                                                                                       76.78;
                                                                                                                                                                                                          OTHER INFORMATION: 2363327
                                                                                                                                                                                                                                                                                       Local Similarity 99.6
nes 728; Conservative
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                                                                                                                                                TYPE: PRT
ORGANISM: Homo
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600 878 099 720

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APVOESPPLAMPGNSHGLEVGSLAEVKENPPFYGVIRWIGQPPGLNEVLAGLELEDECA
                                            GOKVODCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKDFKL
                                                                       481 GOKVODCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAFSCLIIQMPRFGKDFKL
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TITLE OF INVENTION:

FILE REPERENCE: 784FLPCT:

CURRENT APPLICATION NOWEL NUCleic Acid and Polypeptides
FILE REPERENCE: 784FLPCT:

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US/99/488,725

PRIOR PELICATION NUMBER: US/99/552,317

PRIOR APPLICATION NUMBER: US/99/552,317

PRIOR PLING DATE: 2000-04-25

PRIOR PLING DATE: 2000-06-20

PRIOR PELING DATE: 2000-06-20

PRIOR PELING DATE: 2000-06-20

PRIOR PELING DATE: 2000-06-31

PRIOR PELING DATE: 2000-09-14

PRIOR PELING DATE: 2000-09-14

PRIOR PELING DATE: 2000-09-14

PRIOR PELING DATE: 2000-09-14

PRIOR PELING DATE: 2000-10-19

PRIOR PELING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 7144

SOFTWARE: DE FL GENEE DE VOERSIONE 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2399, Application US/09488725A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity 99.7
683; Conservative
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US-09-488-725A-2399
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Best Local S:
Matches 683
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APPLICANT: OTA, TOSHIO
APPLICANT: SIGGAI, TAKAO
APPLICANT: SIGGAI, TAKAO
APPLICANT: SIGGAI, TAKAO
APPLICANT: MISHIKAWA, TETSUO
APPLICANT: SAITO, KOJI
APPLICANT: SAITO, KAORU
APPLICANT: SAITO, MAGNU
APPLICANT: SHIL, SHIZUKO
APPLICANT: SHILON
APPLICANT: WAKAMATSU, AI
APPLICANTON WWBERS: US/09/629,469A
PRIOR APPLICATION WWBER: JP 2000-01-28
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 2000-02-17
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CURRENT APPLICATION NUMBER: US/10/258,898A
CURRENT FILING DATE: 2002-10-29
PRIOR PILICATION NUMBER: US/99/488,725
PRIOR PILICATION NUMBER: US/99/552,317
PRIOR PILIOR DATE: 2000-01-21
PRIOR PILIOR DATE: 2000-06-25
PRIOR PILIOR DATE: 2000-06-20
PRIOR PILIOR DATE: 2000-06-20
PRIOR PILIOR DATE: 2000-06-30
PRIOR PILIOR DATE: 2000-06-31
PRIOR PILIOR DATE: 2000-09-14
PRIOR PILIOR DATE: 2000-10-19
PRIOR PILIOR DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7143
SEQ ID NO S: 7143
SEQ ID NO S: 2399
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US-10-258-898A-2399
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Job time : 193 secs
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Sequence 250, App
Sequence 154, App
Sequence 154, App
Sequence 118, App
Sequence 118, App
Sequence 118, App
Sequence 118, App
Sequence 1100, Ap
Sequence 1100, Ap
Sequence 112, App
Sequence 1142, App
Sequence 1142, App
Sequence 1142, App
Sequence 1142, App
Sequence 115, App
Sequence 157, App
Sequence 157, App
Sequence 157, App
Sequence 157, App
Sequence 161, App
Sequence 157, App
Sequence 161, App
Sequence 151, App
Sequence 21, Appl
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(gn12 6/ptodata/1/paa/US06_NEW_COMB.pep:*)

(gn12 6/ptodata/1/paa/US08_NEW_COMB.pep:*)

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(gn12 6/ptodata/1/paa/US09_NEW_COMB.pep:*)

(gn12 6/ptodata/1/paa/US10_NEW_COMB.pep:*)
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-491-213-8
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US-10-491-213-9
US-10-469-740-145
US-10-489-740-145
US-10-81-801-777
US-09-716-964B-118
US-09-716-964B-118
PCT-US04-07412-1099
PCT-US04-07412-1099
PCT-US04-07412-1132
US-10-453-372-1132
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US-10-821-801-752
US-10-821-801-752
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US-09-999-167-161
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Maximum Match 100%
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APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Breleigh, Deepa
APPLICANT: Breleigh, Deepa
TITLE ON INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
FILE REFERENCE: 5152
CURRENT APPLICATION WUMBER: PCT/USO4/07268
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US 60/450,655
PRIOR PILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 254
SOFTWARE: Patentin version 3.2
SEQ ID NO 250
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163, App
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114, App
144, App
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                                             US-60-556-841-10921

US-10-695-499-191

US-10-767-471-1200

US-10-767-471-1200

PCT-US04-09049-5

PCT-US04-07626-53

PCT-US04-07626-53

PCT-US04-07626-53

PCT-US04-07188-112

US-10-764-425-112

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99.5%; Pred. No. 0;
iive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 250, Application PC/TUS0407268 GENERAL INFORMATION:
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Best Local Similarity 99.5
Matches 948; Conservative
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TILE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 786TP4
CURRENT APPLICATION NUMBER: US/10/290,752
CURRENT APPLICATION NUMBER: PCT/US01/04926
PRIOR APPLICATION NUMBER: PCT/US01/04926
PRIOR PILING DATE: 2001-02-26
PRIOR PELING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-14
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US-10-290-752-230
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GENERAL INFORMATION:
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Byeleigh, Deepa
APPLICANT: Bigwood, Douglas
TILE OF INVENTION: EXPRESSION PROFILES FOR BREZ;
FILE REFERENCE: 515.
CURRENT APPLICATION NUMBER: US/10/788,792
CURRENT APPLICATION NUMBER: US 60/450,655
PRIOR APPLICATION NUMBER: US 60/450,655
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US-10-788-792-250
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LENGTH: 960
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APPLICANT: BBERHARDT, INES
APPLICANT: BUTTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: LUYTEN, WALTER HERMAN
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REPERBENCE: JAB-1667
CURRENT APPLICATION NUMBER: US/10/451,467A
PRIOR APPLICATION NUMBER: EP 00870318.3
                 PRIOR FILING DATE: 2001-10-05

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: US 60/329,690

PRIOR FILING DATE: 2001-10-12

PRIOR FILING DATE: 2001-10-26

PRIOR FILING DATE: 2001-10-26

PRIOR PILING DATE: 2001-10-26

PRIOR PRILING DATE: 2001-11-02

PRIOR PILING DATE: 2001-11-02

PRIOR PILING DATE: 2001-11-09

PRIOR FILING DATE: 201-11-09

PRIOR FILING DATE: 201-11-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 KLKSCRPDSRF-----ASLQPVSNQIERCNSLAFGGYLSEVVEENTPPKMEKEGLEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 DPGNRRSELFYTL--NGSSVD-SQPQSKSKNT--WYIDEVAED----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.4%; Score 122.5; DB 6; 23.0%; Pred. No. 1; ive 42; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No: 71863981CD1
US-10-491-213-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 154, Application US/10451467A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PERL Program SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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US-10-451-467A-154
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Best Local S
Matches 83
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CURRENT APPLICATION NUMBER: US/10/491,213
CURRENT FILING DATE: 2004-03-26
PRIOR APPLICATION NUMBER: PCT/US02/31095
PRIOR FILING DATE: 2002-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---PTLPLMKSGDALKQGQEEGR-----LGGGLAPDTSKSCDPGVTGLNK---NRRS 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ELFYTLNG-SSVDSQPQSKSKNTWYID-----EVAEDPAKSLTEISTDFD 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      718 SGCSPRDSGCYESSENLENGKTRKASLLSAKSSTEPSLKSFSRNOLGNY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97;
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APPLICANT: BAUGHN, Mariah R.; BECHA, Shanya D.;
APPLICANT: BOROWSKY, Mark L.; CHAWLA, Narinder K.;
APPLICANT: ELICOTT, VICKI S.; EMERLING, Brooke M.;
APPLICANT: GANDHI, Ameena R; GIETZEN, Kimberly J.;
APPLICANT: GORVAD, Ann E.; GRIFFIN, Jennifer A.;
APPLICANT: HAPALIA, APRIJ J.A.; ISON, Craig H.;
APPLICANT: KABLE, Amy E.; KALAFUS, Daniel P.;
APPLICANT: MARSON, Particia M.; Ju, Dayung Aina M.;
APPLICANT: MARGON, Particia M.; Ju, Dayung Aina M.;
APPLICANT: MARGUNG, Jayalaxmi; RICHARDSON, Thomas W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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TANG, Y. Tom; TRAN, Uyen K.;
WARREN, Bridget A.; XU, Yuming;
                                                                                                                                                                                                                                                                                                                                                                                                     2.7%; Score 134.5; DB 6;
23.1%; Pred. No. 0.21;
ative 44; Mismatches 132;
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YUE, Henry
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APPLICATION NUMBER: US 60/327,380
FILING DATE: 2001-10-05
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PRIOR APPLICATION NUMBER: 09/597,707
PRIOR FILING DATE: 2000-06-17
PRIOR PELING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR PLING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR APPLICATION NUMBER: 09/515,126
PRIOR PLING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 688
SOFTWARE: Custom
SEQ ID NO 230
LENGTH: 1247
TYPE: PRI
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US-10-290-752-230
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----IYGYV 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINTLRKCYPQFAERDSQGGF-YKQQDAEELFTQLFHSMSIVFGDKFSEDFRIQFKTTIK 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 YSVEKKISRLPKFLTVQYVRFFWKRSTNKKSKILRKVVFPPQLDVADMLTPEYAAEKVKV 356
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GENERAL INFORMATION:
APPLICANT: EICHMULLER, STEFAN
APPLICANT: SCHADENDORF, DIRK
APPLICANT: USENER, DIRK
APPLICANT: USENER, DIRK
TITLE OF INVENTION: NOVEL MARKER FOR THE DIAGNOSIS AND THERAPY OF TUMORS
FILE REFERENCE: 38485-0014
CURRENT APPLICATION NUMBER: US/10/416,330
CURRENT FILING DATE: 2003-05-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
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                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 499;
0.63;
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 01870002.1
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 732
SOFWARE: Patentin version 3.1
SEQ ID NO 154
LENGTH: 499
                                                                                                                                                                                                                                                                                                                                                                     2.4%; Score 120;
17.9%; Pred. No. 0
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Matches 101; Conservative
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US-10-451-467A-154
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US-10-416-330-39
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017 QEKHQLLKQQLKDQYFMQRHQLLKRHEKETEQMQRYNQRLIEELKNRQTQERARLPK--- 1073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NRLSKG----LQIDVGCPVKVQLRSGEEKFPGVVR-FRGPLL-AERTVSGIFFGVELLE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGRGOGFTDGVYQGKQLFQCDEDCGFVALDKLE-LIEDDDTALE----SDYAGPGDTMQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      701
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801 DGVEVSVTTSKIVTDSDSKTEELRF----LRRQELRELRFLQKEEQRAQ-QQLNSKLQQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 TSDPGNRRSELFYTLNGSSVDSQPQSKSKNTWYID-EVAEDPA--KSLTEISTDFDRSSP
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                                                                                                                                                                                                                                         Query Match 2.3%; Score 116; DB 6; Length 12
Best Local Similarity 18.5%; Pred. No. 4.9;
Matches 171; Conservative 143; Mismatches 362; Indels
                                                                                                                                                                                                                                                                                                                                                               32 DKQTQKLLKVPKG-----SIGQYIQDRSVGHSRIPSAKGKK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHAVLFVDEDVVEINEKFTELLL-AITNCEERFSLFKNR----
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NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver.
                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-10-416-330-39
                                                           SEQ ID NO 39
LENGTH: 1235
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Conservative
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; SEQ ID NO 777
; LENGTH: 903
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-821-801-777
                                                                                                                                   Best Local Similarity
Matches 80; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 EVVTNGETTCSENGVSLC--LPRLE-----SAI 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GLSDSPISASRVAGFTGASONDDGSRSKDETRVS 217
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TITLE OF INVENTION: Human nucleic acid sequences from lung tumours
FILE REFERENCE: 00154/002011.
CURRENT APPLICATION NUMBER: US/10/821,801
CURRENT PILING DATE: 2004-09-09
PRIOR APPLICATION NUMBER: DE 103 16 701.3
PRIOR PILING DATE: 2003-04-09
NUMBER OF SEQ 1D NOS: 990
SOFTWARE: PatentIn version 3.2
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                                                                                                         Sequence 145, Application US/10489740
GENERAL INFORMATION:
APPLICANT: Bionomics Limited
TILE OF INVENTION: P9
FILE REFERENCE: Anglogenesis PCT
CURRENT APPLICATION NUMBER: US/10/489,740
CURRENT FILING DATE: 2004-03-15
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Version 3.1
SOFTWARE: 903
LENGTH: 903
 Sequence 777, Application US/10821801
GENERAL INFORMATION:
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Brummendorf, Thomas
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Ropcke, Stefan
Mennerich, Detlev
Kinnemann, Henrik
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Hermann, Klaus
Heiden, Esmeralda
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                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-489-740-145
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 80; Conserv
                                                                                             US-10-489-740-145
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APPLICANT:
APPLICANT:
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APPLICANT:
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GAREALL INCORMATION:

GAREALL INCORMATION:

GAREALL INCORMATION:

GAREIGANT: Vuzhakov, Alexander

APPLICANT: Yuzhakov, Alexander

APPLICANT: Yuzhakov, Alexander

APPLICANT: Yuzhakov, Olga

APPLICANT: Yuzhakov, Olga

APPLICANT: Yuzhakov, Irina

APPLICANT: Bruck, Irina

APPLICANT: Bruck, Irina

APPLICANT: Bruck, Irina

APPLICANT: Kuriyan, John

TITLE OF INVENTION: USE THEREOF

FILE REPERENCE: 22221/1030

CURRENT APPLICATION NUMBER: US/09/716,964B

CURRENT FILING DATE: 1997-04-08

FRIOR FILING DATE: 1997-04-08

FRIOR APPLICATION NUMBER: 09/057,416

FRIOR APPLICATION NUMBER: 09/057,416

FRIOR APPLICATION NUMBER: 09/057,416

FRIOR FILING DATE: 1998-04-08

NUMBER OF SEQ ID NOS: 212

SOFTWARE: PALENTING DATE: 1998-04-08

NUMBER OF SEQ ID NOS: 212

SEQ ID NO 118

LENGTH: 1161
                                                                                                                               232
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Length 903;
                                                               Indels
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2.3%; Score 115.5; DB 6; 25.3%; Pred. No. 3.3; tive 35; Mismatches 102;
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17.7%; Pred. No. 5.7;
                                                                                                                                                                                                                                                                                                                       147 EVVTNGETTCSENGVSLC--LPRLE------
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EDNITDKYNHHLILIAKDD------
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Best Local Similarity 17.7%; Pro
Matches 193; Conservative 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     452 PLAMPPG----NSHG 462
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328 ---LPPGWEQRVDQHG 340
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APPLICANT: O'Donnell, Michael E. APPLICANT: Yuzhakov, Alexander
                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                 US-10-671-106-118
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                                             -----NRN--RLSKGLQIDVGCPVKVQLRSGEEKFPGVVRFRGPLLAERTVSGIFFGVE 165
                                                                                                                                      DDTALE----SDYAGPGDTMQVELPP----LEINSRVSLKG-GETIESGTV-----247
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--EERFSLFK
                                                                                         LLEEGRGOGFTDGVYQGKQLFQC-DEDCGF-
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PAPPLICANT: YUZINAKOV, ALEXANUELI
APPLICANT: YUZINEVA, Olga
APPLICANT: Jeruzalni, David
APPLICANT: Jeruzalni, David
APPLICANT: Bruck, Irina
APPLICANT: Kuriyan, John
TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
TITLE OF INVENTION: PUNCTION AS A CHROMOSOWAL REPLICASE, PREPARATION AND
TITLE OF INVENTION: FUNCTION AS A CHROMOSOWAL REPLICASE, PREPARATION OFFICE TOWENT APPLICATION NUMBER: US/10/671,106
CURRENT PILING DATE: 2003-09-25
FRIOR APPLICATION NUMBER: 06/143,202
PRIOR FILING DATE: 1997-04-08
PRIOR APPLICATION NUMBER: 06/143,202
PRIOR APPLICATION NUMBER: 06/143,202
PRIOR APPLICATION NUMBER: 06/143,202
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1997-04-08
PRIOR FILING DATE: 1998-04-08
NUMBER OF SEQ ID NOS: 212
SOFTWARE PARENT PARENTIN OFFICE TOWENT PARENT PARE
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Sequence 118, Application US/10671106
GENERAL INFORMATION:
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564 VPLYYDKEGEVATQYDMVQLEELGLLKMDFLGLKTLTELKLMKELIKERHGVDINFLELP 623
                                                                                                                                                                                                    588 QGHYNSCYLDSTLFCLFAF-----SSVLDTVLLRPKEKNDVEY-YSETQELLRTEIVNP 640
                                                                                                                                                                                                                                                                           641 LRIYG-YVCATKIMKLRKILEKVEAASGFTSEEKD-------PEEFLNIL 682
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                                                      KENPPFYGVIRWIGOPPGLNEVLAGLELEDECAGCTDGTF----RGTRYFTCALKKALFV 527
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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 822CIP/PCT
FILE REPERENCE: 2011/PCT
CURRENT FILING DATE: 2004-03-19
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GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
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PRIOR FILING DATE: 2003-03-14
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 10/296,115
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                                                                                                                                                                653 -LKKLKPDS-----
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Chen, Rui-hong
Wehrman, Tom
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985 TPI---EDLEEWD 994
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Zhou, Ping
Ma, Yunqing
Ghosh, Malabika
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Wang, Zhiwei
Boyle, Bryan J.
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Wang, Jian-rui
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Asundi, Vinod
Zhao, Qing A.
Wang, Dunrui
                                                                                        524 LDDPKVYKLLQ-
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APPLICANT:
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PRIOR FILING DATE: 2000-12-25

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-21

PRIOR PLING DATE: 2000-01-21

PRIOR PLING DATE: 2001-01-25

PRIOR PLING DATE: 2001-01-25

PRIOR PLING DATE: 2000-01-21

PRIOR PLING DATE: 2000-01-25

PRIOR PLING DATE: 2000-01-25
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IG DATE: 2000-12-22
CATION NUMBER: PCT/US00/35017
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Drmanac, Radoje T.
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Chen, Rui-hong
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Ma, Yunqing
Ghosh, Malabika
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Best Local Similarity 22.14
Matches 67; Conservative
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Wang, Jian-rui
Zhang, Jie
Ren, Feiyan
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Zhao, Qing A.
Wang, Dunrui
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Wang, Zhiwei
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ORGANISM: Homo sapiens
PCT-USO4-07412-1100
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GST 487
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ORGANISM: Homo
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CURRENT APPLICATION NUMBER: PCT/US04/07412
CURRENT PILING DATE: 2004-03-19
FRIOR APPLICATION NUMBER: PCT/US04/07412
FRIOR APPLICATION NUMBER: US 10/389,559
FRIOR PILING DATE: 2003-03-14
FRIOR PILING DATE: 2003-03-14
FRIOR PELICATION NUMBER: US 60/340,187
FRIOR APPLICATION NUMBER: US 60/340,187
FRIOR APPLICATION NUMBER: PCT/US00/35017
FRIOR APPLICATION NUMBER: PCT/US00/35017
FRIOR APPLICATION NUMBER: PCT/US00/35017
FRIOR APPLICATION NUMBER: US 09/552,317
FRIOR APPLICATION NUMBER: US 09/552,317
FRIOR APPLICATION NUMBER: US 09/552,317
FRIOR PILING DATE: 2000-01-22
FRIOR PILING DATE: 2000-01-21
FRIOR FILING DATE: 2000-01-21
FRIOR PILING DATE: 2000-01-25
FRIOR APPLICATION NUMBER: US 09/491,404
FRIOR APPLICATION NUMBER: US 09/491,404
FRIOR APPLICATION NUMBER: US 09/491,404
FRIOR FILING DATE: 2000-01-25
FRIOR APPLICATION NUMBER: US 09/491,404
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; Pred. No. 8.1;
42; Mismatches 117; Indels 85;
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APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Zhi Weil
APPLICANT: Trannanc, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
OF INVENTION: Novel Nucleic Acids and Polypeptides
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Best Local Similarity 21.5%
Matches 67; Conservative
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APPLICANT: Tang, Y. Tom
APPLICANT: Hu, Tianhua
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ORGANISM: Homo sapiens
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SEQ ID NO 1099
LENGTH: 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 PHAVLFVDEDVVEINEKF------TELLLAITNCEERFSLFKNRNRLSKGLQIDV 126
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FILE REFERENCE: 824CIP/PCT
CURRENT APPLICATION NUMBER: PCT/USO4/09202
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: US 60/458,824
PRIOR FILING DATE: 2003-03-28
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 10/275,027
PRIOR PILING DATE: 2001-01-25
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-05-17
PRIOR FILING DATE: 2001-05-18
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845 VSSKEFLOTESPESTELOSRLRQLSLLWEAAQGAVDSWRGGLRQSLMQCQ-DFHQLSQNL 903
                                                                                                                          LL-----RPKEKNDVEYYSETQELLRTEIVNPLRIYGYVCATKIMKLRKILEKVEAAS 666
                                                                                                                                                                                                                      -----TPPKMEKEG----LEIMIGKKKGIQGHYNSCYLDSTLFCLFAFSSVLDTV 613
                                                                                                                                                                                                667 GFTSEEKDPEEFLNILFHHILRVEPLLKIRSAGQKVQDCYFYQIFMEKNEKVGV--PTIQ 724
                                                                                                                                                  Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 1920
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PPLICANT: Drmanac, Radoje T.
ITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
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PRIOR APPLICATION NUMBER: US 60/340,187
PRIOR PILING DATE: 2002-03-14
PRIOR PLING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 10/296,115
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-04-25
PRIOR PELING DATE: 2000-04-25
PRIOR PELING DATE: 2000-01-21
PRIOR PELING DATE: 2000-01-21
PRIOR PELING DATE: 2001-01-25
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CURRENT FILING DATE: 2004-03-19
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PRIOR APPLICATION NUMBER: US 60/365,264
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Chen, Rui-hong
Wehrman, Tom
Weng, Gezhi
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Ma, Yunqing
Ghosh, Malabika
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Wang, Jian-rui
Zhang, Jie
Ren, Feiyan
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Asundi, Vinod
Zhao, Qing A.
Wang, Dunrui
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LENGTH: 2404
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                    725 QLLE 728
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APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERARBUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODE FILE BEPERENCE: 21402-589 ACURENT APPLICATION NUMBER: 05/10/453,372
CURRENT APPLICATION NUMBER: 09/789390
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                              443 NT-----APVQESPPLAMPP--GNSHGLEVGSLAEVKENPPFYGVIRWIGQPPGLN 491
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                                                                                                                                                                                     389 -- DRSSPPLQPPPVNSLTT - ENRFHS - - - LPFSLTKMPNTNGSIGHSPLSLSAQSVMEEL
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                                                                          Gaps
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                                                                      Indels 197;
   Length 2404;
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Query Match 2.2%; Score 110.5; DB 1;
Best Local Similarity 19.3%; Pred. No. 34;
Matches 134; Conservative 100; Mismatches 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     897 POVTPCPEVGEYLKMSLEDLHSLD-SRRIQGCARR 930
                                                                                                                                        352 NGSSVDSQPQSKSKN-TW--YIDEVAEDPAKSLTEIST-
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2411 VŠSLVTTITGSSLRGEPMSYYIASGNLGNTFQIDQLTGQVSISQPLDFEKIQKYVVWIEA 2470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2067 TLTGTDIIQVFAADGDEGTNGQV------RYGIVNGNTNQEFRIDSVTGAITVAKPL 2117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---- 2157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------PNSELHYSLSGRNSEKFHIDPLRGALMAAGP 2356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVVEINEKFTELLLAITN-CEERFSLFKNRNRLSKGLOIDVGCPVKVQLRSGEEKFPGVV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 RFRGPLLAERTVSGIFFGVELLEEGRGQGFTDGVYQGKQLFQCDEDCGFVALDKLELIED 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDTALE--SDYAGPGD---TMQVELPPLEINSRVSLKGGETIE-----SGTVIFCDVL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGKESLGYFVGVDM----DNPIGNWDGRFDGVLCSFACVESTILLHINDIIPESVTQERR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----LNGSSVDSQPQS------KSKNTWYIDEVAE 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKENPPFYGVIRWIGQ 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 DKQTQKLLKVPKGSIGQYIQ-----DRSVGHSRIPSAKGKKNQIGLKILEQPHAVLFVDE 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YLSEVVEENTPPKMEKEGLEI-MIGKKK
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PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR PILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR APPLICATION NUMBER: 09/86376
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
PRIOR PILING DATE: 2000-05-31
PRIOR PELING DATE: 2000-05-31
PRIOR PELING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-25
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
2.2%; Score 110; DB 6; Length 4913;
Best Local Similarity 18.1%; Pred. No. 1.18+02;
Matches 176; Conservative 130; Mismatches 332; Indels 334;
                                                                                                                                                                                                                                                                SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 1142
LENGTH: 4913
                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-1142
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Sequence 7, Appli
Sequence 13, Appl
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Sequence 4, Appli
Sequence 6983, Ap
Sequence 18, Appl
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Patent No. 5206163
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US-08-999-774A-12
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Copyright (c) 1993 - 2004
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Sequence 6, Appl: Sequence 2, Appl: Sequence 769, Ap

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 SLTEISTDF---DRSSPPLOPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQ 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------WGGKTDIDLAVDENGLWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 58, Application US/09262537
Patent No. 6479256
GERRAL INFORMATION:
APPLICANT: Hayflick, Joel
TITLE OF INVENTION: Lectomedin Materials and Methods
FILE REPERENCE: 27866/35307
CURRENT PILING DATE: 1999-03-04
EARLIER APPLICATION NUMBER: 60/076,782
EARLIER APPLICATION NUMBER: 60/076,782
SARLIER APPLICATION NUMBER: 60/076,782
SARLIER PILING DATE: 1998-03-04
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
                                                                                        US-09-000-062-3
US-08-945-144A-3
US-08-9107-532A-6065
US-09-107-532A-6065
US-09-107-847-2
US-08-885-291-55
US-08-885-291-2
US-09-496-672-2
US-09-496-672-2
US-09-618-425-11
US-09-159-340A-2
US-09-306-998-3
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US-09-306-998-3
US-09-355-214-3
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20.7%; Pred. No. 0.054;
ive 80; Mismatches 220;
US-09-489-039A-9182
US-09-976-594-726
                                                                   US-09-243-374-5
US-09-000-062-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 LRTRIKSGETV-INTANYHDTSPYR-
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 I-----ERCNSLA-----FGGYLSEVVEENTPPKMEKEGLEIMIGKKKGIQ- 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      589 -----GHYNSCYLDSTLFCLFAFSSVLDTV--LLRPKEKNDVEYYSETQELLRTEIVN 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLRIYGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAG 699
                                                                                             -----TATMIL---DVLE--EGAFILADNVREPARFLAAKQNVVLEVTVL----STE 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             328 HNKPKATGSTSDPGNRRSELFYTLNG----SSVDSQPQSKSKNTW--YIDEVAEDPAKS 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 VMEELN-----TAPVQESPPLAMPPGNSHGLEVGSLAEVKENPPFYGVIRWIGQPPGLN 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      446 AINQLGPDLPPATAP---APSTRRPPAPNLHVSPELFCEPRE------VRRVQWP---- 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  492 EVLAGLELEDECAGCTDGTFRGTRYFTCALKKALF----VKLKSCRPDSRFASLQPVSNQ 547
589 IERESAGKNYNKMHKRERT-CKDYIKAVVETVDNLLRP-----EALESWKDMNATEQVH 641
                                                            640 PLRIYGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSAG 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 FACVESTILLHINDIIPESVTQE-----RRPPKLAFMSRG------VGDKGSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 LTEISTDF---DRSSPPLOPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPLSLSAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 GNRVDYAFNTN--ANREEPVSLAFPNPYQFVSSVDYNPRDNQLYVWNNYF-----
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCRWATION:
APPLICANT: PETERKO, Alexandre
APPLICANT: PETERKO, Alexandre
TITLE OF INVENTION: CALCIUM INDEPENDENT RECEPTOR OF ALPHA-LATROTOXIN,
TITLE OF INVENTION: CHARACTERIZATION AND USES THEREOF
FILE REPERENCE: 1049-1-007
CURRENT APPLICATION NUMBER: US/08/811,519B
CURRENT FILING DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 2.4%; Score 118.5; DB 4; al Similarity 20.6%; Pred. No. 0.25; 117; Conservative 80; Mismatches 207;
                                                                                                                                                                         725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        700 OKVODCYFYQIF-MEKNEKVGVPTIQQ 725
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                                                                                                                                                                         700 QKVQDCYFYQIF-MEKNEKVGVPTIQQ
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08811519B Patent No. 6630345
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TYPE: PRT
ORGANISM: rat
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US-08-811-519-1
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Best Local S:
Matches 117
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                                                                                                                                                                            -----GHYNSCYLDSTLFCLFAFSSVLDTV--LLRPKEKNDVEYYSETQELLRTEIV 638
                                                                                                                                                                                                                                        640
                                                                                                                                                                                                                                                                                            NPLRIYGYVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIRSA 698
                                                                                                                                                                                                                                                                                                                                   :: | | :: :| | :: :| | :: :| HATMLL---DVLE--EGAFILADNVREPARFLAAKENVVLEVTVL---NTE 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVSLKGGETIESGTVIFCDVLPGKESLGYFVGVDMDNPIGNWDGRFD------GVLCS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTRIKSGETV-INTANYHDTSPYR--------WGGKTDIDLAVDENGLWVI 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FACVESTILLHINDIIPESVTQE-----RRPPKLAFMSRG------VGDKGSSS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HNKPKATGSTSDPGNRRSELFYTLNG----SSVDSQPQSKSKNTW--YIDEVAEDPAKS 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 AINQLGPDLPPATAP---APSTRRPPAPNLHVSPELFCEPRE-----VRRVQWP---- 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548 I-----ERCNSLA------FGGYLSEVVEENTPPKMEKEGLEIMIGKKKGIQ- 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GHYNSCYLDSTLFCLFAFSSVLDTV--LLRPKEKNDVEYYSETQELLRTEIVN 639
                                                            QI-----ERCNSLA-----FGGYLSEVVEENTPPKMEKEGLEIMIGKKKGIQ 588
                                                                                          EVLAGLELEDECAGCTDGTFRGTRYFTCALKKALF----VKLKSCRPDSRFASLQPVSNQ
                                                                                                                                                                                                                   Gaps
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GNRVDYAENTN--ANREEPVSLAFPNPYQEVSSVDYNPRDNQLYVWNNYF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09262537
Patent No. 6479256
GENERAL INFORMATION:
APPLICANT: HAPYflick, Joel
TILE REPERENCE: 27866/35307
CURRENT APPLICATION NUMBER: US/09/262,537
CURRENT FILING DATE: 1999-03-04
EARLIER APPLICATION NUMBER: 60/076,782
SARLIER PILING DATE: 1998-03-04
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                               GOKVODCYFYQ-IFMEKNE-KVGVPTIQQ 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GQ-VQELVFPQEEYPRKNSIQLSAKTIKQ 712
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CITY: Chicago
STATE: Illinois
COUNTY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
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Balissa, Harriet
Van Litempt, Henr
Montenegro, Eduardo P.
Marynion: A Method for Influencing Beta-Lactam
VENTION: Antibiotic Production and for Isolation of Large
VENTION: Quantities of ACV Synthetase
                                                                                                                                                                                                                     APPLICANT: Rhodes, Kenneth
APPLICANT: Betty, Maria
APPLICANT: Ling, Huai-Ping
APPLICANT: Ling, Huai-Pi
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300 South Wacker Drive
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EARLIER FILING DATE: 1998-11-20
EARLIER FILING DATE: 1999-04-23
EARLIER FILING DATE: 1999-04-23
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
EARLIER FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: USSN 60/110,277
EARLIER FILING DATE: 1998-11-30
EARLIER APPLICATION NUMBER: USSN 60/110,033
EARLIER FILING DATE: 1998-11-25
                                                                                           -09-399-913-57
Sequence 57, Application US/09399913
Patent No. 6361971
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Barredo, Jose L.
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Garcia, Bruno D.
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SEQ ID NO 57
LENGTH: 267
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ADDRESSEE: McDonnell
STREET: 300 South Wa
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
Matches 46; Conserv
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 E-----VALDEGRGQGFTDGVYQGKQLFQCDEDCGF----VALDKLELIEDDDTAL
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                                                                  PatentIn Release #1.0, Version #1.25
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                                    SOFTWARE: Patentim ...
SOFTWARE: Patentim ...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
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2.3%; Sc
Best Local Similarity 18.5%; Pr
Matches 145; Conservative 109;
IBM PC compatible
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287 LEDPLEFLDMAEIKEKICDYLFNVSDSSALNLAKNIGLTKARDINAVLIDMERQGDVYRQ 346
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  188 EAGTPPLWKIAVSTQAWNQHSGVVRP-----DGHSQGAPNSDPSLEP-----EDRNST 235
                                                                                               236 SVSEDLLEPFIAVSAQAWNQHSGVVRPDSHSQGSP----NSDPGLEPED----SNSTSA 286
                                                                                                                                                 357 DSQP-----QSKSKNTWYIDEVAEDPAKSLTE------ISTDFDRSSPPLQ- 396
                                                                                                                                                                                                                                              397 --PPPVNSLTTENR-----FHSLP------FSLTKMPNTNGS---IGH 428
                                                                                                                                                                                                                                                                                       347 GTTPPIWHLTDKKRERMQIKRNTNSVPETAPAAIPETKRNAEFLTCNIPTSNASNNMVTT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 PDDLNSIRA------APGEFR-----AIMEMPSFYSHGLPRCSFYKKLTECQLK 502
                                                  SVTQERRPPKLAFMSR-----GVGDKGSSSHNKPKATGSTSDPGNRRSELFYTLNGSSV
                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5677428
GENERAL INFORMATION:
APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600 LFCLFAFSSVLDTVLLRPKEKN-DVEYYSETQELLRT 635
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-JUL-1994
ATTORNEY AGENT INFORMATION:
NAME: BAK, MARY E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: WST49CUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
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IBM PC compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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STATE: P.
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 VALDKLELIEDDDTA----LESDYAGPGDTM-----QVELPPLEINS----RVSLKGGETI 242
: || || || AGQYLCAYYISQQEATPAQ----LRDYAAQKLPAYMLPSYFVKLDKMPLTPNDKIDRKAL 511
                                                                        ----LEKVEAASGFTSEEKDPEEFLNILFHHILRVEPLLKIR------SAGQKVQ 703
                                                                                                            PEPDLTANQSQAAYHPPRTETESILVSIWQNVLGIEK-IGIRDNFYSLGGDSIQAIQVVA 570
                                                                                                                                                                                                      128 SHFQELSIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKGKLQK 187
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                                                                                                                                                                        ---APSCLIIQMPRFG 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08280443
Patent No. 5643778
GENERAL INFORMATION:
APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                      704 DCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAE-----
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,443
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
ATTOCNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 215-540-9206
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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RESULT 9
PCT-US95-02275-2
; Sequence 2, Application PC/TUS9502275
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                                                                                                                                                                      287 LEDPLEFLDMAEIKEKICDYLFNVSDSSALNLAKNIGITKARDINAVLIDMERQGDVYRQ
                                                                                                                                                                                                                                                                                                                                                                                                            236 SVSEDLLEPFIAVSAQAWNQHSGVVRPDSHSQGSP-----NSDPGLEPED----SNSTSA
                                                                                                                                                   142 PGVVRFRGP-LLAERT----VSGIFFGVELLEEGRGQGFTDGVYQGKQLFQCDEDCGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKKALFVK--LKSCRPDSRFASLQ--
                                                                                                                 Gaps
                                                                          ; Score 113; DB 1; Length 1226;
; Pred. No. 0.62;
81; Mismatches 249; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nishikura, Kazuko
TITLE OF INVENTION: RNA Editing Enzyme and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSE: HOWSON and HOWSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600 LFCLFAFSSVLDTVLLRPKEKN-DVEYYSETQELLRT 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Howson and Howson
Spring House Corporate Cntr, P.O. Box
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5763174
                                                                        2.2%;
                                                                                             Best Local Similarity 19.9%
Matches 115; Conservative
TOPOLOGY: linear
MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Spring House
STATE: Pennsylvania
                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                      US-08-457-459-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-555-678-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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236 SVSEDILIEPFIAVSAQAWNQHSGVVRPDSHSQGSP----NSDPGLEPED----SNSTSA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 LEDPLEFLDMAEIKEKICDYLFNVSDSSALNLAKNIGLTKARDINAVLIDMERQGDVYRQ 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 SHFQELSIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKGKLQK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESGTVIFCDVLPGKESLGYFVGVDMDNPIGNWDGRFDGVLCSFACVESTILLHINDIIPE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVTQERRPPKLAFMSR-----GVGDKGSSSHNKPKATGSTSDPGNRRSELFYTLNGSSV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 --PPPVNSLTTENR----FHSLP-----FSLTKMPNTNGS---IGH 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 GTTPPIWHLTDKKKERMQIKRNTNSVPETAPAAIPETKRNAEFLTCNIPTSNASNNMVTT 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 EKVENGQEPVIKLENRQEARPEPARLKPPVHYNGPSKAGYVDFENG-----QWATDDI 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     429 SPLSLSAQSVMBELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKENPPFYGVIRWIGQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 PGVVRFRGP-LLAERT-----VSGIFFGVELLEEGRGQGFTDGVYQGKQLFQCDEDCGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 VALDKLELIEDDDTA----LESDYAGPGDTM----QVELPPLEINS---RVSLKGGETI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.2%; Score 113; DB 1; Length 1226;
19.9%; Pred. No. 0.62;
tive 81; Mismatches 249; Indels 132; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           600 LFCLFAFSSVLDTVLLRPKEKN-DVEYYSETQELLRT 635
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,794
FILING DATE: 17-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/280,443
FILING DATE: 25-UL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,459
FILING DATE: 01-UNN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST49DUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1226 amino acids
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Best Local Similarity 19.9
Matches 115; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                          543 -PVSNQIERCNSLAFGGYLSE--VVEENTPPKMEKEGLEIMIGKKKGIQGHYNSCYLDST 599
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                       487 PPGLNEVLAGLELEDECAGCTDGTFRGTRYFTCALKKALFVK--LKSCRPDSRFASLQ-- 542
                                                                        ----APGEFR----AIMEMPSFYSHGLPRCSPYKKLTECQLK 502
                                                                                                                                                                         503 NPISGLLEYAQ---FASQTCEFNMIEQSGPPHEPRFKFQVVINGREFPPAEAGSKKVAKQ 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | :| ||:
32 GLDSTGYY-----DQEIYGGSDSRFAGYVTSIAATELEDDDDDYSSSTSLLGQKKPGYHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gish, Kurt C.
APPLICANT: Sequezi, Wolfgang
APPLICANT: Shanahan, Frances
APPLICANT: Lees, Emma M.
APPLICANT: McClanahan, Terrill K.
TITLE OF INVENTION: Intracellular Regulatory Molecules;
TITLE OF INVENTION: Related Reagents
                                                                                                                                                                                                                          600 LFCLFAFSSVLDTVLLRPKEKN-DVEYYSETQELLRT 635
                                                                                                                                                                                                                                                       560 DAAMKAMTILLEEAKAKDSGKSEESSHYSTEKESEKT 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.2%; Score 112.5; DB 3;
23.1%; Pred. No. 0.14;
iive 32; Mismatches 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/999,774A FILING DATE: 10-DEC-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,818
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08999774A
Patent No. 6274312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34,090
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (650)852-9196
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Best Local Similarity 23.1%
Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ching, Edwin P. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                        460 PDDLNSIRA----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-999-774A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-999-774A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PG-LRPRFPVILLASSTRGRQVDIRGVPRGVHLGSQGLQRGFQHPSPRGRSLPQRGVDCLS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 VALDKLELIEDDDTA----LESDYAGPGDTM-----QVELPPLEINS---RVSLKGGETI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 SHFQELSIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKGKLQK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESGTVIFCDVLPGKESLGYFVGVDMDNPIGNWDGRFDGVLCSFACVESTILLHINDIIPE 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVTQERRPPKLAFMSR-----GVGDKGSSSHNKPKATGSTSDPGNRRSELFYTLNGSSV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVSEDILEPFIAVSAQAWNQHSGVVRPDSHSQGSP----NSDPGLEPED----SNSTSA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 DSQP-----QSKSKNTWYIDEVAEDPAKSLTE------ISTDFDRSSPPLQ- 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 LEDPLEFLDMAEIKEKICDÝLFNÝSDSSALNLAKNIGLTKARDINAVLIDMERQGDVYRQ 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407 EKVENGQEPVIKLENRQEARPEPARLKPPVHYNGPSKAGYVDFENG------QWATDDI 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.2%; Score 113; DB 5; Length 1226; 19.9%; Pred. No. 0.62;
               APPLICANT: Wister Institute of Anatomy &, Biology
TITLE OF INVENTION: RNA Editing Enzyme and Methods of Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
                                                                                                                               ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION WUMBER:
FILING DATE: 25-UJL-1994
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/197,794
FILING DATE: 17-FBB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET WUMBER: WST49BPCT
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 215-540-9206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PPPVNSLTTENR-----FHSLP
                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1226 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    datches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215-540-5818
                                                                                                                                                                                                                                                                         ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR
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                                                                                                                                                                                                                                               COUNTRY:
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-AKIEIKDTTGK 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                589 GHYNSCYLDSTLFCLFAFSSVLDTVLLRPKEKNDVEY-----YSETQELLRTEIVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      506 CT-DGTFRGTRYFTCALKKALFVKLKSCRPDSRFASLQPVSNQIERCNSLAFGGYLSEVV
                                                                                                        565 E----ENTPP-KMEKEGLEIMIGKKKGIQGHYNSCYLDSTLFCLFAFSSVLDTVLLRPK
                                                                                                                              ---AITAGSETDDARPK
                                                                                                                                                                                                              547 LTGSGEANA-----TLTTYDNGVAIGVVTVTSGRSWSFTFDKDLALGKHTITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 VTQERRPPKLAFMSRGVGDKGS-SSHNKPKATGSTSDPGNRRSELFYTLNGSSVDSQPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 LTKTSQNPDLDLISLDSDDEGAKSSSLQDKGLSSTKKP--KRFPVLLTAQ-TSKDPEDPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 KSKNTWYIDEVAEDPAKSLTEISTDFDRSSPPL--QPPPVNSLTTENRFHSLPFSLTKMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 PSEVDW--DGLEDEAAKY-----HNPDWPPFLTRPPPYNKATP----SAP-TVMAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 NTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGN---SHGLEVGSLAEVKENPPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 YGVIRWIGQPPGLNEVLAGLELEDE-----CAGCTDGTFRGTRYFTCALKKALFVKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          531 SCRPDSRFASLOPVSNQIERCNSLAFGGYLSEVVEEN--TPPKMEKEGLEIMIGKKKGIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 PGLFAQIQAAATKAWRKLPVKGDPGASLTGVKQGPDEPFADFVHRL------ITTAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 KVQDCYFYQIFMEKNEKVGVPTIQQLLEWSFINSNLKFAEAPSCLIIQMPRFGKD----
                                                                    ----AGNKSEVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 NPKEELKEKIAQLEEQIKLEELHQALISKLOKL--KTGNETVTHPDTAGGLSRTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 143; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09370368
Patent No. 6258932
GENERAL INFORMATION:
APPLICANT: Anders Vahlne
TITLE OF INVENTION: AND METHODS OF USE THEREOF
TITLE OF INVENTION: AND METHODS OF USE THEREOF
                                                         463 VIGSGTADANGKFTISISPAL-----TDNKHASVSAIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Mismatches 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 2.2%; Score 110.5; Di Similarity 20.2%; Pred. No. 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: TRIPED.003A
CURRENT APPLICATION NUMBER: US/09/370,368
CURRENT FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                              425 FDSIAPDKPTVQINTDGTSVTGTAEAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mason-Pfizer Monkey Virus
US-09-370-368-7
                                                                                                                                                                                                                                                                                     612
                                                                                                                                                                                                                                                  660 EKVEAASGFTSEEKDPEEF 678
                                                                                                                                                                                                                                                                        Matches 112; Conservative
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PB
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                       424
                                                                                                       197 KRRW--DQTADQTPGATPKKLSSWDQAETPGHTPSLRWDETPGR-----AKGSETPG 246
                                                                                                                                         474
                                                                                                                                                                 247 ATPGSKIWDPTPSHTPAGAA------TPGRGDTPGHATPG--HG---GATSSARKN 291
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                                  138 DGGKTPDPKMNARTYMDVMREQHLTKEEREIRQQLAEKAKAGELKVVNGAAA-SQPPSKR 196
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 --FYTLNGSSVDSQPQSKS 364
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                                                                     KNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPVNSLTTENRFHSLPFSLTKMPNTNG
                                                                                                                                           SI-----GHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.2%; Score 112; DB 4; Length 734;
20.0%; Pred. No. 0.31;
tive 95; Mismatches 264; Indels 232;
                                                                                                                                                                                                               PPFYGVIRWIGQPPGLNEVLAGLELEDECAGCTDGTFRGTRY 516
                                                                                                                                                                                                                                                  -----RWDETPKTERDTLG----HGSGWGETPRTDRGGDY 322
                                                                                                                                                                                                                                                                                                                                     Sequence 4412, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Acinetobacter baumannii
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 --GSTSDPG-NRRSEL-
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Best Local Similarity
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365 KNTWYIDEVAEDPAKSLTEISTDFDRSSPPLQPPPVNSLTTENRFHSLPFSLTKMPNTNG 424
                                                                                      -----GHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKEN 474
                                                                                                                   ----TPGRGDTPGHATPG--HG---GATSSARKN
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1998-12-04
APPLICATION NUMBER: PCT/US98/11422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/205,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1998-06-04
APPLICATION UNDBER: 60/048,885
APPLICATION DATE: 1997-06-06
APPLICATION NUMBER: 60/049,375
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APPLICATION NUMBER: 60/048,916
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/048,876
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APPLICATION NUMBER: 60/048,895
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APPLICATION NUMBER: 60/048,882
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APPLICATION NUMBER: 60/048,899
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APPLICATION NUMBER: 60/048,892
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APPLICATION NUMBER: 60/049,019
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APPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/048,884
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APPLICATION NUMBER: 60/048,894
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APPLICATION NUMBER: 60/048,964
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APPLICATION NUMBER: 60/048,901
                                                                                                                                                                                                                                                                                                                             Sequence 689, Application US/09205258 Patent No. 6525174
                                                                                                                            247 ATPGSKIWDPTPSHTPAGAA
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                                                                                                                                                                            475 PPFYGVIRWIGQP 487
                                                                                                                                                                                                                       ------RWDETP 297
                                                                                      425 SI---
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US-09-205-258-689
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756 FKLFKKIFPSLE-----LNITDLLEDTPRQCRICGGLAMYECRECYDDPDISAG 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 DGGKTPDPKMNVRTYMDVMREQHLTKEEREIRQQLAEKAKAGELKVVNGAAA-SQPPSKR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509 IRLCSDIGPSYQQGLAMAAAFSGQTVKDFLNNKNKEKGGC------CFKC-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255 GKESLGYFVGVDMDNPI-GNWDGRFDGVLCSFACVE-----STILL-----H-
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                                                                                                                                                                                                                                                                                                    APPLICANT: Seghezzi, Wolfgang
APPLICANT: Seghezzi, Wolfgang
APPLICANT: Shanahan, Prances
APPLICANT: Shanahan, Prances
APPLICANT: McClanahan, Terrill K.
APPLICANT: McClanahan, Terrill K.
TITLE OF INVENTION: Intracellular Regulatory Molecules;
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/999,774A FILING DATE: 10-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.2%; Score 109.5; Best Local Similarity 23.0%; Pred. No. 1.5 Matches 72; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: DNAX Research Institute
STREET: 901 Callfornia Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,818
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         Sequence 13, Application US/08999774A Patent No. 6274312 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
marss: not relevant
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1306 amino acids
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(650)496-1200
                                                                                      KIKQFCKTCNTQVH 818
                                                                                                                                 KKGHFAKNCHEHAH 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-999-774A-13
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302 ESVIQERRPPKLAFMSRGVGDKG-----SSSHNK-PKATGSTSDPG-NRRSELFYTLN 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 EDVK--PPVLGV-RGLHCPPPPGGPGGRRL---CAICGDRS-SGKHYGVYSCEGCKGFF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 VKL------KSCRPDSRFASLQPVSNQIERCNSLAF-----GGYLSEVVEENTP 569
266 -----PAVS-SVLSTGV--PTVPLLPPQVNQSLTSVPPMNPATTLPGLMPLPAGLPN 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 PFSLTKMPNTNGSIGHSPLSLSAQSVMEELNTAPVQESPPLAMPPGNS----HGLEVGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: LEID, MARK
APPLICANT: KASTNER, PHILIPPE
APPLICANT: CHAMBON, PIERRE
APPLICANT: CHAMBON, PIERRE
TITLE OF INVENTION: NOVEL HETERODIMERIC STEROID RECEPTOR
TITLE OF INVENTION: PROTEINS, GENES ENCODING SAME, AND USAGE THEREOF
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21.5%; Pred. No. 0.43;
tive 56; Mismatches 163; Indels 230;
                                                                                    419 MPNTNGSIGHSPLSLSAQSVMEELNTAPVQES--PPL-AMPPGNSHGL 463
                                                                                                                              315 LPNLN-----LNLPAPHIMPGVGLPELVNPGLPPLPSMPPRNLPGI 355
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APPLICATION NUMBER: US/08/216,592A
FILING DATE: 23-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue NW Suite 600 CITY: Washington
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/825,667
FILING DATE: 24-JAN-1992
ATTORNEY AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1383.00600(
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08216592A
Patent No. 6635429
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IBM PC compatible
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Sterne, K
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STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                            -08-216-592A-4
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Best Local
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, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-205-258-689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 FTELLLAITNCEERFSLFKNRNRLSKGLQIDVGCPVKVQLRSGEEKFPGVVRFRGPLLAE 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 RTVSGIFFGVELLEEGRGQGFTDGVYQGKQLFQCDEDCGFVALDK-----LELIEDDDTA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 SNLWG------GQGL------GQGL------LGVSIRFCSFDGANENVWHVLEVESNSPAA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 L----ESDYAGPGDTMQVELPPLEINSRVSLKGGETIESGTVIFCDVLPGKESLGYFVG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 LAGLRPHSDYIIGADTVMNESEDL----FSLI--ETHEA-------KPLKLYVYN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 VDMDN-----PIGNWDGRFDGVLCSFACVESTILLHINDIIPESVTQERR----PPKL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 AF-----MSRGVGDKGSSSHNKPKATGSTSDPGNRRSELFYTINGSSVDSQPQSKSKNTW 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PPVNSLTTENRFHSLPFSLTK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 LKVPKGSIGQY----IQDRSVGHSRIPSAKGKKNQIGLKILEQPHAVLFVDEDVVEINEK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :::| | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | :: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | 
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23.3%; Pred. No. 0.26;
tive 46; Mismatches 151; Indels 162;
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                                                                                                                      APPLICATION NUMBER: 60/049,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
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EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                      APPLICATION NUMBER: 60/048,917
                                                                                                                                                                                                                                                                                      60/048,949
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EARLIER FILING DATE: 1997-06-06
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Matches 109; Conservative
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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ORGANISM: Homo sapiens
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LOCATION: (61)
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Search completed: April 28, 2004, 10:14:01 Job time : 25 secs